SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Hanna, Nabil

Newman, Roland A. Reff, Mitchell E.

- (ii) TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human Therapy
- (iii) NUMBER OF SEQUENCES: 59
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 - (B) STREET: 699 Prince Street
 - (C) CITY: Alexandria
 - (D) STATE: VA
 - (E) COUNTRY: USA
 - (F) ZIP: 22314-3187
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/523,894
 - (B) FILING DATE: 06-SEP-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Teskin, Robin L.
 - (B) REGISTRATION NUMBER: 35,030
 - (C) REFERENCE/DOCKET NUMBER: 012712-165
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 703-836-6620
 - (B) TELEFAX: 703-836-2021
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 420 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Monkey

(A) CHROMOSOME/SEGMENT: light variable domain of CE9.1 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 4..420 (ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 61..420 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: GAC ATG AAA CAC CTG TGG TTC TTC CTC CTG GTG GCA GCC CCC AGA 48 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg -15 TGG GTC TTG TCC CAG GTG CAG CTG CAG GAG GCG GGC CCA GGA CTG GTG 96 Trp Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Gly Leu Val AAG CCT TCG GAG ACC CTG TCC CTC ACC TGC AGT GTC TCT GGT GGC TCC 144 Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser 15 20 ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA GGG AAG 192 Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys 30 GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGG GGC ACC AAT 240 Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn 45 50 TAC AAT CCC TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC 288 Tyr Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser 70 AAG AAC CTC TTC TCC CTG AAA CTG AGG TCT GTG ACC GCC GCG GAC ACG 336 Lys Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr 85 GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT CAC TGG TTA 384 Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu 95 105 TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC 420 Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser 110 115 120

(2) INFORMATION FOR SEQ ID NO:2:

(Viii) POSITION IN GENOME:

N

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
-19 -15 -10 -5

Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Gly Leu Val Lys
1 5 10

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile 15 20 25

Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly 30 35 40 45

Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr
50 55 60

Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys
65 70 75

Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala 80 85 90

Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu 95 100 105

Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser 110 115 120

- (2) INFORMATION FOR SEQ ID NO:3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Monkey
 - (Viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: heavy variable domain of CE9.1
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 4..387
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 61..387

		(xi)	SEC	QUENC	CE DI	ESCRI	PTIC	on: s	SEQ :	D NO	0:3:						
	ACC						CTG Leu										48
	GAC Asp	TCT Ser	GCG Ala	GCC Ala	TCC Ser 1	TAT Tyr	GAG Glu	TTG Leu	AGT Ser 5	CAG Gln	CCT Pro	CGC Arg	TCA Ser	GTG Val 10	TCC Ser	GTG Val	96
							GGG Gly										144
1 · 1							TAC Tyr 35									GTG Val	192
then the and that							AGC Ser										240
	TTC Phe	TCT Ser	GGC Gly	TCC Ser	AAC Asn 65	TCA Ser	GGG Gly	AAC Asn	ACC Thr	GCC Ala 70	ACC Thr	CTG Leu	ACC Thr	ATC Ile	AGC Ser 75	GGG	288
oli ili ilian iliafi							GCT Ala										336
P Test Gall																CTA Leu	384
	GGT Gly																387

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp
-19 -15 -10 -5

Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser 1 5 10

Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly Arg
15 20 25

Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val Leu 30 40 45

Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe
50 55 60

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val 65 70 75

Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Thr 80 85 90

Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly 95 100 105

- (2) INFORMATION FOR SEQ ID NO:5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: lambda variable and constant domains in CE9.1
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..702
 - (ix) FEATURE:
 - (A) NAME/KEY: mat peptide
 - (B) LOCATION: 1..702
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
- ATG GCC TGG GCT CTG CTC CTC GGC CTC CTT GCT CAC TTT ACA GAC

 Met Ala Trp Ala Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp

 1 5 10 15
- TCT GCG GCC TCC TAT GAG TTG AGT CAG CCT CGC TCA GTG TCC GTG TCC

 Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser

 20 25 30
- CCA GGA CAG ACG GCC GGG TTC ACC TGT GGG GGA GAC AAC GTT GGA AGG 144

	Pro	Gly	Gln 35	Thr	Ala	Gly	Phe	Thr 40	Cys	Gly	Gly	Asp	Asn 45	Val	Gly	Arg		
							CAG Gln 55											192
							GAA Glu										•	240
							AAC Asn											288
2 5 11							GAC Asp									ACT Thr		336
							GGC Gly											384
1							TCG Ser 135											432
That He show Shall							GCC Ala											480
Tenfi Tenfi							GTG Val											528
							ACC Thr											576
							CTG Leu											624
							CAG Gln 215											672
							GAA Glu											702

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 amino acids

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Trp Ala Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp
1 5 10 15

Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser 20 25 30

Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly Arg

Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val Leu 50 60

Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe
65 70 75 80

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val 85 90 95

Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Thr 100 105 110

Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly 115 120 125

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu 130 135 140

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe 145 150 155 160

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val 165 170 175

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys 180 185 190

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser 195 200 205

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu 210 215 220

Lys Thr Val Ala Pro Thr Glu Cys Ser * 230

- (2) INFORMATION FOR SEQ ID NO:7:
 - (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 1404 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: heavy chain variable and constant gamma

48

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1404

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	Met	Lys	His	Leu	Trp 5	Phe	Phe	Leu	Leu	Leu 10	. Val	GCA Ala	GCC Ala	CCC Pro	AGA Arg 15	TGG Trp	•	48
	GTC Val	TTG Leu	TCC Ser	CAG Gln 20	val	CAG Gln	CTG Leu	CAG Gln	GAG Glu 25	Ser	GGC Gly	CCA Pro	GGA Gly	CTG Leu 30	GTG Val	AAG Lys		96
	CCT Pro	TCG Ser	GAG Glu 35	ACC	CTG Leu	TCC	CTC Leu	ACC Thr 40	Cys	AGT Ser	GTC Val	TCT Ser	GGT Gly 45	GGC Gly	TCC Ser	ATC Ile		144
	AGC Ser	GGT Gly 50	GAC Asp	TAT Tyr	TAT	TGG Trp	TTC Phe 55	TGG Trp	ATC Ile	CGC Arg	CAG Gln	TCC Ser 60	CCA Pro	GGG Gly	AAG Lys	GGA Gly		192
	CTG Leu 65	GAG Glu	TGG Trp	ATC Ile	GGC Gly	TAC Tyr 70	ATC Ile	TAT Tyr	GGC Gly	AGT Ser	GGT Gly 75	GGG Gly	GGC Gly	ACC Thr	AAT Asn	TAC Tyr 80		240
	AAT Asn	CCC Pro	TCC Ser	CTC Leu	AAC Asn 85	AAT Asn	CGA Arg	GTC Val	TCC Ser	ATT Ile 90	TCA Ser	ATA Ile	GAC Asp	ACG Thr	TCC Ser 95	AAG Lys	•	288
	AAC Asn	CTC Leu	TTC Phe	TCC Ser 100	CTG Leu	AAA Lys	CTG Leu	AGG Arg	TCT Ser 105	GTG Val	ACC Thr	GCC Ala	GCG Ala	GAC Asp 110	ACG Thr	GCC Ala		336
1	GTC Val	TAT Tyr	TAC Tỹr 115	TGT Cys	GCG Ala	AGT Ser	AAT Asn	ATA Ile 120	TTG Leu	AAA Lys	TAT Tyr	CTT Leu	CAC His 125	TGG Trp	TTA Leu	TTA Leu		384
•	rac ryr	TGG Trp	GGC Gly	CAG Gln	GGA Gly	GTC Val	CTG Leu	GTC Val	ACC Thr	GTC Val	TCC Ser	TCA Ser	GCT Ala	AGC Ser	ACC Thr	AAG Lys		432

ATG AAA CAC CTG TGG TTC TTC CTC CTG GTG GCA GCC CCC AGA TGG

		130					135					140					
	GGC Gly 145	Pro	TCC Ser	GTC Val	TTC Phe	CCC Pro 150	CTG Leu	GCG Ala	CCC Pro	TGC Cys	TCC Ser 155	Arg	AGC Ser	ACC Thr	TCC Ser	GAG Glu 160	480
	AGC Ser	ACA Thr	GCC Ala	GCC Ala	CTG Leu 165	GGC Gly	TGC Cys	CTG Leu	GTC Val	AAG Lys 170	Asp	TAC Tyr	TTC Phe	CCC Pro	GAA Glu 175	CCG Pro	528
	GTG Val	ACG Thr	GTG Val	TCG Ser 180	TGG Trp	AAC Asn	TCA Ser	GGC Gly	GCC Ala 185	Leu	ACC Thr	AGC Ser	GGC Gly	GTG Val 190	His	ACC Thr	576
	TTC Phe	CCG Pro	GCT Ala 195	GTC Val	CTA Leu	CAG Gln	TCC	TCA Ser 200	GGA Gly	CTC Leu	TAC Tyr	TCC Ser	CTC Leu 205	AGC Ser	AGC Ser	GTG Val	624
T. C. C. C.	GTG Val	ACC Thr 210	GTG Val	CCC Pro	TCC Ser	AGC Ser	AGC Ser 215	TTG Leu	GGC Gly	ACG Thr	AAG Lys	ACC Thr 220	TAC Tyr	ACC Thr	TGC Cys	AAC Asn	672
The Tark the Hall	GTA Val 225	GAT Asp	CAC His	AAG Lys	CCC Pro	AGC Ser 230	AAC Asn	ACC Thr	AAG Lys	GTG Val	GAC Asp 235	AAG Lys	AGA Arg	GTT Val	GAG Glu	TCC Ser 240	720
	AAA Lys	TAT Tyr	GGT Gly	CCC Pro	CCA Pro 245	TGC Cys	CCA Pro	TCA Ser	TGĆ Cys	CCA Pro 250	GCA Ala	CCT Pro	GAG Glu	TTC Phe	CTG Leu 255	GGG Gly	768
	GGA Gly	CCA Pro	TCA Ser	GTC Val 260	TTC Phe	CTG Leu	TTC Phe	CCC Pro	CCA Pro 265	AAA Lys	CCC Pro	AAG Lys	GAC Asp	ACT Thr 270	CTC Leu	ATG Met	816
	ATC Ile	TCC Ser	CGG Arg 275	ACC Thr	CCT Pro	GAG Glu	GTC Val	ACG Thr 280	TGC Cys	GTG Val	GTG Val	GTG Val	GAC Asp 285	GTG Val	AGC Ser	CAG Gln	864
	GAA Glu	GAC Asp 290	CCC Pro	GAG Glu	GTC Val	CAG Gln	TTC Phe 295	AAC Asn	TGG Trp	TAC Tyr	GTG Val	GAT Asp 300	GGC Gly	GTG Val	GAG Glu	GTG Val	912
	CAT His 305	AAT Asn	GCC Ala	AAG Lys	ACA Thr	AAG Lys 310	CCG Pro	CGG Arg	GAG Glu	GAG Glu	CAG Gln 315	TTC Phe	AAC Asn	AGC Ser	ACG Thr	TAC Tyr 320	960
	CGT Arg	GTG Val	GTC Val	AGC Ser	GTC Val 325	CTC Leu	ACC Thr	GTC Val	CTG Leu	CAC His 330	CAG Gln	GAC Asp	TGG Trp	CTG Leu	AAC Asn 335	GGC Gly	1008
	AAG Lys	GAG Glu	TAC Tyr	AAG Lys 340	TGC Cys	AAG Lys	GTC Val	TCC Ser	AAC Asn 345	AAA Lys	GGC Gly	CTC Leu	CCG Pro	TCC Ser 350	TCC Ser	ATC Ile	1056
	GAG Glu	AAA Lys	ACC Thr	ATC Ile	TCC Ser	AAA Lys	GCC Ala	AAA Lys	GGG Gly	CAG Gln	CCC Pro	CGA Arg	GAG Glu	CCA Pro	CAG Gln	GTG Val	1104

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile

Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly

Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Thr Asn Tyr

20

35

Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys
85 90 95

Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala 100 105 110

Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu 115 120 125

Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys 130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu 145 150 155 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro 165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr 180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn 210 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser 235 240

Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln 275 280 285

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser 370 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val 420 425 430

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460

Leu Gly Lys *

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1404 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: heavy chain gamma 4 with the E mutation
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1404
 - (ix) FEATURE:
 - (A) NAME/KEY: mat peptide
 - (B) LOCATION: 1..1404
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met 1	Lys	His	Leu	Trp 5	Phe	Phe	Leu	Leu	Leu 10	GTG Val	GCA Ala	GCC Ala	CCC Pro	AGA Arg 15	TGG Trp	48
GTC Val	TTG Leu	TCC Ser	CAG Gln 20	GTG Val	CAG Gln	CTG Leu	CAG Gln	GAG Glu 25	TCG Ser	GGC Gly	CCA Pro	GGA Gly	CTG Leu	GTG Val	AAG Lys	96

CCT TCG GAG ACC CTG TCC CTC ACC TGC AGT GTC TCT GGT GGC TCC ATC
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile

35

AGC Ser	GGT Gly 50	Asp	TAT Tyr	TAT	TGG	TTC Phe 55	Trp	ATC Ile	CGC Arg	CAG Gln	TCC Ser 60	Pro	GGG Gly	AAG Lys	GGA Gly		192
CTG Leu 65	ı Glu	TGG Trp	ATC Ile	GGC Gly	TAC Tyr 70	·Ile	TAT	GGC Gly	AGT Ser	GGT Gly 75	GGG Gly	GGC Gly	ACC Thr	AAT Asn	TAC Tyr 80		240
AAT Asn	CCC Pro	TCC Ser	CTC Leu	AAC Asn 85	Asn	CGA Arg	GTC Val	TCC Ser	ATT Ile 90	Ser	ATA Ile	GAC Asp	ACG Thr	TCC Ser 95	AAG Lys	:	288
AAC Asn	CTC Leu	TTC Phe	TCC Ser 100	Leu	AAA Lys	CTG Leu	AGG Arg	TCT Ser 105	Val	ACC Thr	GCC Ala	GCG Ala	GAC Asp 110	Thr	GCC Ala	:	336
GTC Val	TAT	TAC Tyr 115	Cys	GCG Ala	AGT Ser	AAT Asn	ATA Ile 120	Leu	AAA Lys	TAT Tyr	CTT Leu	CAC His 125	TGG Trp	TTA Leu	TTA Leu	;	384
TAC Tyr	TGG Trp 130	GGC Gly	CAG Gln	GGA Gly	GTC Val	CTG Leu 135	GTC Val	ACC Thr	GTC Val	TCC Ser	TCA Ser 140	GCT Ala	AGC Ser	ACC Thr	AAG Lys	4	432
145	Pro	Ser	Val	Phe	Pro 150		Ala	Pro	Cys	Ser 155	Arg	Ser	Thr	Ser	Glu 160	4	180
AGC Ser	ACA Thr	GCC Ala	GCC Ala	CTG Leu 165	GGC Gly	TGC Cys	CTG Leu	GTC Val	AAG Lys 170	GAC Asp	TAC Tyr	TTC Phe	CCC Pro	GAA Glu 175	CCG Pro	5	528
GTG Val	ACG Thr	GTG Val	TCG Ser 180	TGG Trp	AAC Asn	TCA Ser	GGC Gly	GCC Ala 185	CTG Leu	ACC Thr	AGC Ser	GGC Gly	GTG Val 190	CAC His	ACC Thr	. 5	576
TTC Phe	CCG Pro	GCT Ala 195	GTC Val	CTA Leu	CAG Gln	TCC Ser	TCA Ser 200	GGA Gly	CTC Leu	TAC	TCC Ser	CTC Leu 205	AGC Ser	AGC Ser	GTG Val	6	124
vai	210	Val	Pro	Ser	Ser	AGC Ser 215	Leu	Gly	Thr	Lys	Thr 220	Tyr	Thr	Cys	Asn	6	72
GTA Val 225	GAT Asp	CAC His	AAG Lys	CCC Pro	AGC Ser 230	AAC Asn	ACC Thr	AAG Lys	GTG Val	GAC Asp 235	AAG Lys	AGA Arg	GTT Val	GAG Glu	TCC Ser 240	7	20
AAA Lys	TAT Tyr	GGT Gly	CCC Pro	CCA Pro 245	TGC Cys	CCA Pro	TCA Ser	TGC Cys	CCA Pro 250	GCA Ala	CCT Pro	GAG Glu	TTC Phe	GAG Glu 255	GGG Gly	7	68
GGA Gly	CCA Pro	TCA Ser	GTC Val 260	TTC Phe	CTG Leu	TTC Phe	Pro	CCA Pro 265	AAA Lys	CCC Pro	AAG Lys	Asp ·	ACT Thr 270	CTC Leu	ATG Met	8	16

	AT Il	C TC e Se	C CG r Ar 27	ع تت	C CC	r GAC o Gli	G GT(280	Cys	C GTO	G GTO	G GT l Va	G GAC 1 Asp 285	y Vai	G AGO	C CAG		864
	GA: Gl:	A GA u As 29	פ דד	C GAO	G GTO	C CAG	TTC Phe 295	ASI	TGG Trp	TAC Ty	C GTO	GAS 1 As 30	p Gly	GTC Val	GAC Glu	GTG 1 Val		912
•	CA! His		r GC n Al	C AAG a Lys	G ACA	A AAG Lys 310	Pro	CGG Arg	GAG Glu	GAG Glu	CAC Gli Gli	n Phe	C AAC e Asn	AGC Ser	ACC Thi	TAC Tyr 320		960
	Arg	r GTC g Val	G GT	C AGO l Ser	GTC Val 325	. Leu	ACC Thr	GTC Val	CTG Leu	CAC His	Glr	GAC Asp	TGG Trp	CTG Leu	AAC Asr 335	GGC Gly		1008
	AAG Lys	GAC Glu	TAC Ty	Lys 340	, cys	AAG Lys	GTC Val	TCC Ser	AAC Asn 345	AAA Lys	GGC Gly	CTC	CCG Pro	TCC Ser 350	Ser	ATC Ile		1056
	GAG Glu	AAA Lys	ACC Thr 355		TCC Ser	AAA Lys	GCC Ala	AAA Lys 360	GGG Gly	CAG Gln	CCC Pro	CGA Arg	GAG Glu 365	CCA Pro	CAG Gln	GTG Val		1104
	TAC Tyr	ACC Thr 370		CCC Pro	CCA	TCC Ser	CAG Gln 375	GAG Glu	GAG Glu	ATG Met	ACC Thr	AAG Lys 380	Asn	CAG Gln	GTC Val	AGC Ser	٠.	1152
The state of the s	CTG Leu 385	ACC Thr	TGC Cys	CTG Leu	GTC Val	AAA Lys 390	GGC Gly	TTC Phe	TAC Tyr	CCC Pro	AGC Ser 395	GAC Asp	ATC Ile	GCC Ala	GTG Val	GAG Glu 400		1200
= sireg	TGG Trp	GAG Glu	AGC Ser	AAT Asn	GGG Gly 405	CAG Gln	CCG Pro	GAG Glu	AAC Asn	AAC Asn 410	TAC Tyr	AAG Lys	ACC Thr	ACG Thr	CCT Pro 415	CCC Pro		1248
	GTG Val	CTG Leu	GAC Asp	TCC Ser 420	GAC Asp	GGC Gly	TCC Ser	Pne	TTC Phe 425	CTC Leu	TAC Tyr	AGC Ser	AGG Arg	CTA Leu 430	ACC Thr	GTG Val		1296
	GAC Asp	AAG Lys	AGC Ser 435	AGG Arg	TGG Trp	CAG Gln	GIU	GGG Gly 440	AAT Asn	GTC Val	TTC Phe	TCA Ser	TGC Cys 445	TCC Ser	GTG Val	ATG Met		1344
	CAT His	GAG Glu 450	GCT Ala	CTG Leu	CAC His	MOII	CAC His	TAC /	ACA (Thr (CAG . Gln	Lys	AGC Ser 460	CTC (ICC Ser	CTG Leu	TCT Ser		1392
	CTG Leu 465	GGT Gly	AAA Lys	TGA *					·				·					1404

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
- Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
- Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
- Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile
- Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly
- Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr
- Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys
- Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala
- Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu 120
- Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys 135
- Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu 150 160
- Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
- Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
- Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val 200
- Val Thr Val Pro Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn 215
- Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser
- Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Glu Gly 250 -255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln 275 280 285

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser 370 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val 420 425 430

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460

Leu Gly Lys * 465

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1404 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and E mutation

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1404

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATO Met	- Llys	A CAC 5 His	CTG Lev	TGG Trp	TTC Phe	TTC Phe	CTC Lev	CTC Lev	CTC Leu 10	ı Val	GC!	A GCC a Ala	CCC Pro	AGA Arg	TGG Trp		48
GTC Val	TTC Lev	TCC Ser	CAG Gln 20	ı vaı	CAG Gln	CTG Leu	CAG Glr	GAG Glu 25	ı Ser	GGC Gly	CCP Pro	A GGA o Gly	CTG Leu	. Val	AAG Lys		96
CCT	TCG Ser	GAG Glu 35	unr	CTG Leu	TCC Ser	CTC Leu	ACC Thr	. Cys	AGT Ser	GTC Val	TCI Ser	GGT Gly 45	Gly	TCC Ser	ATC Ile		144
AGC Ser	GGT Gly 50	ASP	TAT Tyr	TAT Tyr	TGG Trp	TTC Phe 55	Trp	ATC Ile	CGC Arg	CAG Gln	TCC Ser 60		GGG Gly	AAG Lys	GGA Gly	:	192
CTG Leu 65	GIU	TGG Trp	ATC Ile	GGC Gly	TAC Tyr 70	ATC Ile	TAT	GGC Gly	AGT Ser	GGT Gly 75	GGG Gly	GGC Gly	ACC Thr	AAT Asn	TAC Tyr 80	:	240
AAT Asn	CCC Pro	TCC Ser	CTC Leu	AAC Asn 85	AAT Asn	CGA Arg	GTC Val	TCC Ser	ATT Ile 90	Ser	ATA Ile	GAC Asp	ACG Thr	TCC Ser 95	AAG Lys	. 2	288
AAC Asn	CTC Leu	TTC Phe	TCC Ser 100	CTG Leu	AAA Lys	CTG Leu	AGG Arg	TCT Ser 105	Val	ACC Thr	GCC Ala	GCG Ala	GAC Asp 110	ACG Thr	GCC Ala	3	36
GTC Val	TAT Tyr	TAC Tyr 115	TGT Cys	GCG Ala	AGT Ser	AAT Asn	ATA Ile 120	TTG Leu	AAA Lys	TAT Týr	CTT Leu	CAC His 125	TGG Trp	TTA Leu	TTA Leu	3	84
TAC Tyr	TGG Trp 130	GGC Gly	CAG Gln	GGA Gly	GTC Val	CTG Leu 135	GTC Val	ACC Thr	GTC Val	TCC Ser	TCA Ser 140	GCT Ala	AGC Ser	ACC Thr	AAG Lys	4	32
GGG Gly 145	CCA Pro	TCC Ser	GTC Val	TTC Phe	CCC Pro 150	CTG Leu	GCG Ala	CCC Pro	TGC Cys	TCC Ser 155	AGG Arg	AGC Ser	ACC Thr	TCC Ser	GAG Glu 160	. 4	80
AGC Ser	ACA Thr	GCC Ala	GCC Ala	CTG Leu	GGC Gly	TGC Cys	CTG Leu	GTC Val	AAG Lys	GAC Asp	TAC Tyr	TTC Phe	CCC Pro	GAA Glu	CCG Pro	5	28

					16	5				17	70				17	75	
	GT Va	G AC	G GT I Va	G TC 1 Se: 18	,	G AA	C TC n Se	A GG r Gl	C GC Y Al 18	a Le	G Ac	C AG	c GG	C GT Y Va	al Hi	.C ACC .s Thr	576
			19	5	r ne	a GI	11 Je.	20	0	λ re	u Ty	r Se	r Le 20	u Se 5	r Se	C GTG r Val	624
	GT(Va	G AC 1 Th 21		G CCC	C TCC Ser	C AGO	Sei Sei 21	r re	G GGG	C AC	G AA r Ly	G AC s Th 22	r Ty	C AC r Th	C TG r Cy	C AAC s Asn	672
	225	5			PIC	230	. ASI	ı ını	r Lys	s va	1 As 23	p Ly 5	s Ar	g Va	l Gl	G TCC u Ser 240	720
"" ""	-1	A TAT	r GGT r Gly	CCC Pro	CCA Pro 245	Cys	CCA Pro	CCA Pro	TGC Cys	25	O Al	A CC	GAC	TTO	C GA(e Gl: 25	G GGG u Gly	768
The Table Total	GGA Gly	CCI Pro	A TCA Ser	GTC Val 260	FILE	CTG Leu	TTC Phe	CCC Pro	CCA Pro 265	r.Y.s	A CCC	C AAC	GAC S As	C ACT	r Lei	C ATG	816
H. Brau Start	ATC Ile	TCC Ser	CGG Arg 275		CCT Pro	GAG Glu	GTC Val	ACG Thr 280	Cys	GTG Val	GTO L Val	GTG L Val	GAC Asr 285	Va]	G AGO L Sei	CAG Gln	864
The state of the s	GAA Glu	GAC Asp 290		GAG Glu	GTC Val	CAG Gln	TTC Phe 295	AAC Asn	TGG Trp	TAC	GTG Val	GAT Asp	Gly	GTG Val	GAG Glu	GTG Val	912
	CAT His 305	AAT Asn	GCC Ala	AAG Lys	ACA Thr	AAG Lys 310	CCG Pro	CGG Arg	GAG Glu	GAG Glu	CAG Gln 315	Phe	AAC Asn	AGC Ser	ACG Thr	TAC Tyr 320	960
	CGT Arg	GTG Val	GTC Val	AGC Ser	GTC Val 325	CTC Leu	ACC Thr	GTC Val	CTG Leu	CAC His	CAG Gln	GAC Asp	TGG Trp	CTG Leu	AAC Asn 335	GGC Gly	1008
	AAG Lys	GAG Glu	TAC Tyr	AAG Lys 340	TGC Cys	AAG Lys	GTC Val	TCC Ser	AAC Asn 345	гÀг	GGC Gly	CTC Leu	CCG Pro	TCC Ser 350	TCC Ser	ATC Ile	1056
	GAG Glu	AAA Lys	ACC Thr 355	ATC Ile	TCC Ser	AAA Lys	GCC Ala	AAA Lys 360	GGG Gly	CAG Gln	CCC Pro	CGA Arg	GAG Glu 365	CCA Pro	CAG Gln	GTG Val	1104
		ACC Thr 370	CTG Leu	CCC Pro	CCA Pro	Set	CAG Gln 375	GAG Glu	GAG Glu	ATG Met	ACC Thr	AAG Lys 380		CAG Gln	GTC Val	AGC Ser	1152
	CTG Leu	ACC Thr	TGC Cys	CTG (Leu	GTC /	AAA (Lys (GGC G	TTC (TAC Tyr	CCC Pro	AGC Ser		ATC Ile	GCC Ala	GTG Val	GAG Glu	1200

385					390					395					400	
TGG	GAG Glu	AGC Ser	AAT Asn	GGG Gly 405	CAG	CCG Pro	GAG Glu	AAC Asn	AAC Asn 410	TAC Tyr	AAG Lys	ACC Thr	ACG Thr	CCT Pro 415	CCC	124
GTG Val	CTG Leu	GAC Asp	TCC Ser 420	GAC Asp	GGÇ Gly	TCC Ser	TTC Phe	TTC Phe 425	CTC Leu	TAC Tyr	AGC Ser	AGG Arg	CTA Leu 430	ACC Thr	GTG Val	129
GÀC Asp	AAG Lys	AGC Ser 435	AGG Arg	TGG Trp	CAG Gln	GAG Glu	GGG Gly 440	AAT Asn	GTC Val	TTC Phe	TCA Ser	TGC Cys 445	TCC Ser	GTG Val	ATG Met	134
CAT His	GAG Glu 450	GCT Ala	CTG Leu	CAC His	AAC Asn	CAC His 455	TAC Tyr	ACA Thr	CAG Gln	AAG Lys	AGC Ser 460	CTC Leu	TCC Ser	CTG Leu	TCT Ser	139
	GGT Gly		TGA *													1404

- (2) INFORMATION FOR SEQ ID NO:12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp 1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys 20 25 30

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile 35 40 45

Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly 50 60

Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr 65 70 75 80

Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys
85 90 95

Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala 100 105 110

Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu

	T	yr	Trp	G]	Ly G	ln (Gly	Va	1 L	eu 35	Va	l T	hr '	Va]	L Se	r S	er 1 40	Ala	. S∈	er T	hr	Lys
															13	J				•		Glu 160
•													-	., 0						1	75	Pro
•																			19	0		Thr
æ																	2	05				Val
										-					•	22	U.					Asn
	22														233						- 1	240
	-1										•		2:	30		Pro				25	5	-
												200	•			Lys			270			
										_						Va]	28	של				
·																Asp 300						
												•		-) T D	Phe					3	20
	Arg	Va	11 7	/al	Ser	7a 32	1 I 5	eu	Thr	V	al	Leu	Hi:	s (ln	Asp	Tr	o I	Leu	Asn 335	G	ly
	Lys	G1	.u I	'yr	Lys 340	Су	s L	ys	Val	S	er i	Asn 345	Lys	s G	ly	Leu	Pro	> S 3	er 50	Ser	I	le
	Glu	Ly	s I	hr 55	Ile	Se	- L	ys i	Ala	L)	ys (50	Gly	Glr	ı P	ro.	Arg	Glu 365	ı P	ro	Gln	Va	1
	Tyr	Th:	r L O	eu	Pro	Pro	S	er (31n 375	G1	Lu c	lu	Met	: T	hr :	Lys 380			ln	Val	Se	r
	Leu 385	Thi	ב כֵּ	ys :	Leu	Val	. Ly	ys (90	ly	Ph	le I	Yr	Pro) S	er <i>1</i> 95	4sp	Ile	A.	la '	Val	G1 40	
	Trp	Glı	1 S	er i	Asn	Gly 405	G]	ln F	ro	Gl	u A	sn .	Asn 410	ŢΊ	yr I	Ys	Thr	Tì	ır]	Pro	Pr	0

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val 420 425 430

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460

Leu Gly Lys * 465

- (2) INFORMATION FOR SEQ ID NO:13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human or Monkey
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: VH1 leader sequence

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACTAAGTCGA CATGGACTGG ACCTGG

- (2) INFORMATION FOR SEQ ID NO:14:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human or Monkey
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: VH2 leader sequence

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
ACTAAGTCGA CATGGACATA CTTTGTTCCA C	31
(2) INFORMATION FOR SEQ ID NO:15:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: NO	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey</pre>	
<pre>(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH3 leader sequence</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
ACTAAGTCGA CATGGAGTTT GGGCTGAGC	29
(2) INFORMATION FOR SEQ ID NO:16:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: NO	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey</pre>	
(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH4 leader sequence	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
ACTAAGTCGA CATGAAACAC CTGTGGTTCT T	31
(2) INFORMATION FOR SEQ ID NO:17:	_
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs	

(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey</pre>	
<pre>(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH5 leader sequence</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
ACTAAGTCGA CATGGGGTCA ACCGCCATCC T	3 1
(2) INFORMATION FOR SEQ ID NO:18:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: NO	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey</pre>	
<pre>(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH6 leader sequence</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
ACTAAGTCGA CATGTCTGTC TCCTTCA T	31
(2) INFORMATION FOR SEQ ID NO:19:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: NO	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey	
<pre>(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH1 leader sequence with MluI site</pre>	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	٠
GGCAGCAGCY ACGCGTGCCC ACTCCGAGGT	_
(2) INFORMATION FOR SEQ ID NO:20:	U
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: NO	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey</pre>	
<pre>(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH2 leader sequence with MluI site</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
GACCGTCCCG ACGCGTGTYT TGTCCCAGGT	
(2) INFORMATION FOR SEQ ID NO:21:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: NO	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey</pre>	
(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH3 leader sequence with MluI site	

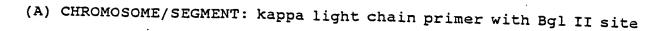
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
GCTATTTCA CGCGTGTCCA GTGTGAG	27
(2) INFORMATION FOR SEQ ID NO:22:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: NO	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey</pre>	
(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH4 leader sequence with MluI site	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
GCGGCTCCCA CGCGTGTCCT GTCCCAG	27
(2) INFORMATION FOR SEQ ID NO:23:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: NO	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey</pre>	
<pre>(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH5 leader sequence with MluI site</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
GGCTGTTCTC ACGCGTGTCT GTGCCGAGGT	80
(2) INFORMATION FOR SEQ ID NO:24:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 23 base pairs	

	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iv)	ANTI-SENSE: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey	·
(viii)	POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH1,3a,5 primer with Xho I site	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:24:	
CAGGTGCA	GC TGCTCGAGTC TGG	23
(2) INFO	RMATION FOR SEQ ID NO:25:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iv)	ANTI-SENSE: NO	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey	
(viii)	POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH2 primer with Xho I site	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:25:	
CAGGTCAAC	CT TACTCGAGTC TGG	23
(2) INFOR	RMATION FOR SEQ ID NO:26:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iv)	ANTI-SENSE: NO	

• •	RIGINAL SOURCE: (A) ORGANISM: Human or Monkey	
	OSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH3b primer with XhoI site	
(xi) S	EQUENCE DESCRIPTION: SEQ ID NO:26:	
GAGGTGCAGC	TGCTCGAGTC TGG	23
(2) INFORM	ATION FOR SEQ ID NO:27:	
	EQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) M	OLECULE TYPE: DNA (genomic)	
(iv) Al	NTI-SENSE: NO	
	OSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH4 primer with XhoI site	
(xi) SE	EQUENCE DESCRIPTION: SEQ ID NO:27:	
CAGGTGCAGC	TGCTCGAGTC GGG	23
(2) INFORMA	ATION FOR SEQ ID NO:28:	
(EQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MC	DLECULE TYPE: DNA (genomic)	
(iv) AN	TI-SENSE: NO	
	RIGINAL SOURCE: (A) ORGANISM: Human or Monkey	
	OSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH6 primer with XhoI site	
(xi) SE	QUENCE DESCRIPTION: SEQ ID NO:28:	

CAGG	ACAGC TGCTCGAGTC AGG	
(2) I	INFORMATION FOR SEQ ID NO:29:	2
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: YES	
(1	vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey	٠
(vi	ii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: IgG1-4 primer with NheI site	
(x	(i) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
	ATGCG CTAGCTGAGG AGACGG	
(2) IN	FORMATION FOR SEQ ID NO:30:	26
	 i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 38 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(i:	i) MOLECULE TYPE: DNA (genomic)	
(it	v) ANTI-SENSE: NO	
iv)	i) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey	
(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: kappa light chain primer with Bgl II site	e
) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
	ATC TCTCACCATG GTGTTGCAGA CCCAGGTC	3
(2) INF	ORMATION FOR SEQ ID NO:31:	
(i)) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iv) ANTI-SENSE: NO (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: kappa light chain primer with Bgl II site (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31: ATCACAGATC TCTCACCATG GRGWCCCCWG CKCAGCT 37 (2) INFORMATION FOR SEQ ID NO:32: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iv) ANTI-SENSE: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: kappa light chain primer with Bgl II site (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32: ATCACAGATC TCTCACCATG GACATGAGGG TCCCCGCTCA G 41 (2) INFORMATION FOR SEQ ID NO:33: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iv) ANTI-SENSE: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey (viii) POSITION IN GENOME:



(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:33:

ATCACAGATC TCTCACCATG GACACVAGGG CCCCCACTCA G

41

- (2) INFORMATION FOR SEQ ID NO:34:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human or Monkey
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: lambda light chain primer with Bgl II site
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ATCACAGATC TCTCACCATG GCCTGGGCTC TGCTGCTCC

- (2) INFORMATION FOR SEQ ID NO:35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iv) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Human or Monkey
 - (viii) POSITION IN GENOME:
 - (A) CHROMOSOME/SEGMENT: lambda light chain primer with Bgl II site
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

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ATCACAGATC TCTCACCATG GCCTGGGCTC CACTACTTC (2) INFORMATION FOR SEQ ID NO:36: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iv) ANTI-SENSE: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: lambda light chain primer with Bgl II (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36: ATCACAGATC TCTCACCATG ACCTGCTCCC CTCTCCTCC 39 (2) INFORMATION FOR SEQ ID NO:37: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iv) ANTI-SENSE: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: lambda light chain primer with Bgl II (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37: ATCACAGATC TCTCACCATG GCCTGGACTC CTCTCTTC 39 (2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iv) ANTI-SENSE: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: lambda light chain primer with Bgl II site (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38: ATCACAGATC TCTCACCATG ACTTGGACCC CACTCCTC (2) INFORMATION FOR SEQ ID NO:39: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iv) ANTI-SENSE: YES (vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey (viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: kappa light chain primer with Kpn1 and BsiW1 sites (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39: CCGTTTGATT TCCAGCTTGG TACCTCCACC GAACGT

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- (2) INFORMATION FOR SEQ ID NO:40:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - _ (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey	
(viii)) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: kappa light chain primer with Kpnl and BsiWl sites	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:40:	
TGCAGCA	TCC GTACGTTTGA TTTCCAGCTT	3
(2) INFO	DRMATION FOR SEQ ID NO:41:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iv)	ANTI-SENSE: YES	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey	
(viii)	POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: lambda light chain primer with HindIII and Kpn1 sites	•
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:41:	
ACCTAGGA	CG GTAAGCTTGG TACCTCCGCC	30
(2) INFO	RMATION FOR SEQ ID NO:42:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iv)	ANTI-SENSE: YES	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey	
(viii)	POSITION IN GENOME:	

(A) CHROMOSOME/SEGMENT: lambda light chain primer with Kpn 1

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:42:	
ACCTAGGA	CG GTCASSTTGG TACCTCCGCC GAACAC	36
(2) INFO	RMATION FOR SEQ ID NO:43:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iv)	ANTI-SENSE: YES	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Human or Monkey	
(viii)	POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: lambda light chain primer with AvrII s	site
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:43:	
	GA CCTAGGACGG TCAGCCG	27
	RMATION FOR SEQ ID NO:44:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iv)	ANTI-SENSE: NO	
	POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH1 heavy chain variable region	·
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:44:	
CCATGGACT	IG GACCTGG	17
(2) INFOR	RMATION FOR SEQ ID NO:45:	

(1)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iv)	ANTI-SENSE: NO	
(viii)	POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH2 heavy chain variable region	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:45:	
ATGGACAT	AC TTTGTTCCAC	20
(2) INFO	RMATION FOR SEQ ID NO:46:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: DNA (genomic)	
(iv)	ANTI-SENSE: NO	
(viii)	POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH3 heavy chain variable region	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:46:	
	TT TGGGCTGAGC	20
(2) INFOR	RMATION FOR SEQ ID NO:47:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<u>(</u> ii)	MOLECULE TYPE: DNA (genomic)	
(iv)	ANTI-SENSE: NO	
(viii)	POSITION IN GENOME:	

(A) CHROMOSOME/SEGMENT: VH4 heavy chain variable region	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:	
ATGAAACACC TGTGGTTCTT	
(2) INFORMATION FOR SEQ ID NO:48:	20
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: NO	
(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH5 heavy chain variable region	
(vi) SECURIVO	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:	
ATGGGGTCAA CCGCCATCCT	20
(2) INFORMATION FOR SEQ ID NO:49:	. •
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: NO	
<pre>(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: VH6 heavy chain variable region</pre>	
(vi) SECURIVE	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:	
ATGTCTGTCT CCTTCCTCAT	
(2) INFORMATION FOR SEQ ID NO:50:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 base pairs	

(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: Kappa light chain variable region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:	
GATGACCCAG TCTCCAKCCT C	21
(2) INFORMATION FOR SEQ ID NO:53:	21
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: Lambda light chain variable region	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
CTCAYTYRCT GCMCAGGGTC C	21
(2) INFORMATION FOR SEQ ID NO:54:	21
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	
(iv) ANTI-SENSE: YES	
(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: kappa light chain constant region	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	
AAGACAGATG GTGCAGCCA	19
(2) INFORMATION FOR SEQ ID NO:55:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: DNA (genomic)	

	(iv) ANTI-SENSE: YES	
	(viii)) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: lambda light chain constant region	1
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:55:	
	GGÀACAGA	AGT GACCGAGGG	
	(2) INFO	RMATION FOR SEQ ID NO:56:	20
1, 878 14 Part	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<u>1</u>]]] =L	(ii)	MOLECULE TYPE: DNA (genomic)	
	(viii)	POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: PCR primer for human gamma 4 constant region	
Tool took ludt for stone Bull	GGGGGGATC	SEQUENCE DESCRIPTION: SEQ ID NO:56:	30
		MATION FOR SEQ ID NO:57:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) 1	MOLECULE TYPE: DNA (genomic)	
	(viii) I	POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: PCR primer for Human gamma 4 constant region	
	(xi) s	EQUENCE DESCRIPTION: SEQ ID NO:57:	
C		ACCAAGGCC CATCCGTCTT C	
		ATION FOR SEQ ID NO:58:	31

(A) LENGTH: 96 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: PCR mutagenesis of human gamma 4
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:
CCGGGAGATC ATGAGAGTGT CCTTGGGTTT TGGGGGGAAC AGGAAGACTG ATGGTCCCCC
CTCGAACTCA GGTGCTGGGC ATGGTGGCA TGGGGG
(2) INFORMATION FOR SEQ ID NO:59:
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(viii) POSITION IN GENOME: (A) CHROMOSOME/SEGMENT: PCR mutagenesis of human gamma 4
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
TCCTCAGCTA GCACCAAGGG GCCATCC